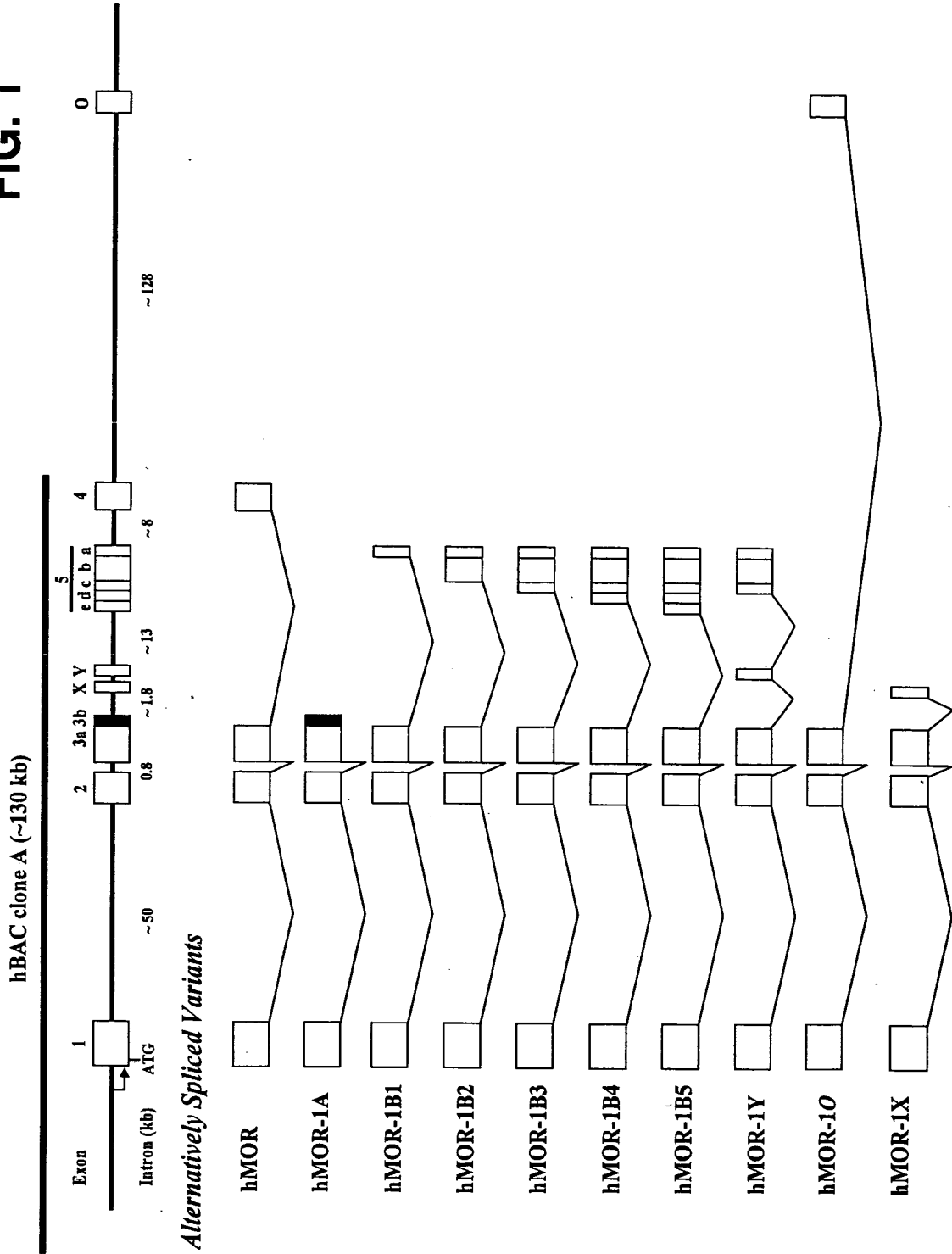


Genomic Structure of the human mu opioid receptor gene

FIG. 1



hMOR-1A

Exon 3a ↓ Exon 3b
---ACTAATCATCAGGTACGCAGTCTCTAGAAATTAGGTATATCTACTGGGGATGACATAAAAATTATAAGGCTT
T N H Q V R S L * (SEQ ID NO:27)
TGTGCTAAACTAGGAGTTTAATCCATTATAGAGGATGAGAATGGAGGAAGAGGGAAGCAAGGG (SEQ ID NO:28)

hMOR-1B1

Exon 3a ↓ Exon 5a
---ACTAATCATCAGAAAAATAGATTTTATTTCAAAAGTCATCTTTACTCAACTGTGAGCATAACCAAGGGCTAATA
T N H Q K I D L F Q K S S[#] L L N C E H T K G * (SEQ ID NO:29)
ATTACAATATTTTCCCGTGAAAGAATATAAGATTGGAAGC (SEQ ID NO:30)

hMOR-1B2

Exon 3a ↓ Exon 5b
---ACTAATCATCAGAGAGAAAGAAAGACAGAAAATCTGACTGGTAAGAAATTTGTACCCTTTTGCCAGCATGCCA
T N H Q R E R R Q K S[#] D W * (SEQ ID NO:31)
GGCTTCTGGGTTCCCTTTCCCTGAGCGGGCCCTAGTGATCCGGCTTGCGGCACCATCGCCTACGGGCC--- (SEQ ID NO:32)

hMOR-1B3

Exon 3a ↓ Exon 5c
---ACTAATCATCAGGGACCTCCAGCCCAAGTTTGTGTGACCAACTTGCCGGGTCTGTCTTGAAAAGGGGCTT
T N H Q G P P A K F V A D Q L A G S S * (SEQ ID NO:33)
ACAGGTGTTCCAAGCCCGTGTATTATCCTGAAGTATCCCTCAACACAGAAAAACGACCTCATAACACAAAA--- (SEQ ID NO:34)

hMOR-1B4

Exon 3a ↓ Exon 5d
---ACTAATCATCAGAGCTGACTATGACATGAACCCCTAAAAATTCCTGTTCCTCC--- (SEQ ID NO:35)
T N H Q S * (SEQ ID NO:36)

FIG. 1B(1)

hMOR-1B5

Exon 3a ↓ Exon 5e
---ACTAATCATCAGGTGGAATTGAACCTGGACTGTCACTGTGAAAATGCAAAGCCCTTGGCCCACTGAGCTACAA
T N H Q V E L N L D C H C E N A K P W P L S Y^f N
TGCAGGGTAGTCTCCATTTCCTTCCCAGGAAGAGTCTAGAGCGTTA--- (SEQ ID NO:37)
A G * (SEQ ID NO:38)

hMOR-1Y

Exon 3a ↓ Exon Y
---ACTAATCATCAGATCAGAGATCCAATATCAAAACCTTCCCAGGGTGTCTGTATTCTGACAACTGTCCACTGA
T N H Q I R D P I S N L P R V S[#] V F * (SEQ ID NO:39)
↓ Exon 5c
GGCAATTTCATACAGCGCAAAAGTGGAGTGGCGATTGGCAGTTATCAAGGGGACCTCCAGCCCAAGTT TGTT--- (SEQ ID NO:40)

FIG. 1B(2)

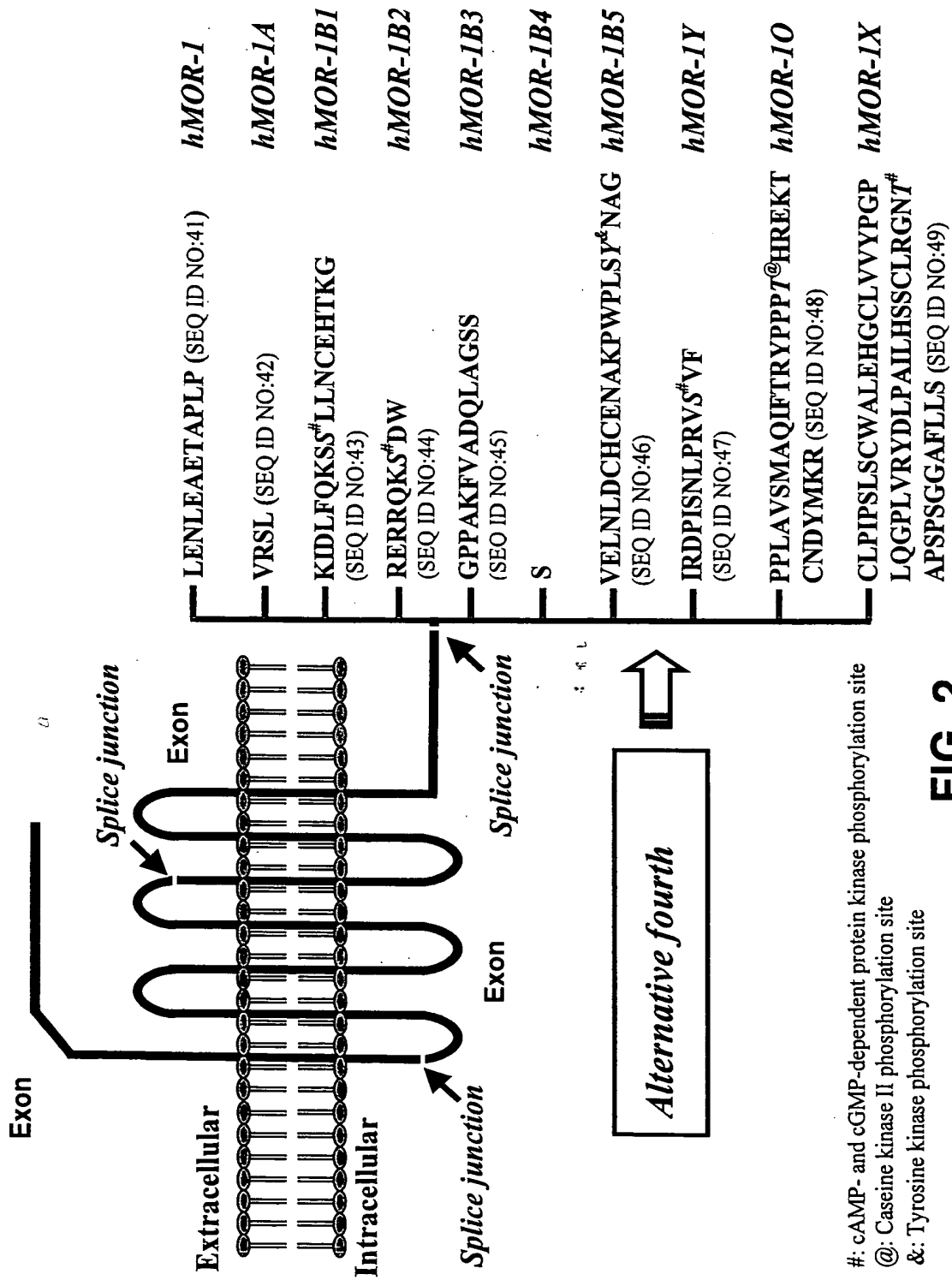


FIG. 2

hMOR-1B1 (1354 bp)

CGGAAAGGAAGCGGCTGAGCGCTTGGAACCCGAAAAAGTCTCGGTGCTCCTGGTACCTCGCACAGCGGTGCCCCGCC
GGCCGTACGTACCATGGACAGCAGCGCTGCCCCACGAACGCCAGCAATTGCACTGATGCCTTGGGTACTCAAGTTG
CTCCCAGACCCAGCCCGGTTCTGTGGTCAACTTGTCCCACCTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAAC
CGCACCGACCTGGCGGGAGAGACAGCCCTGTGCCCTCCGACCGGAGTCCCTCCATGATCAGGCCATCAGATCATG
GCCCTCTACTCCATCGTGTGCGTGGGGCTCTTCGGAACCTTCCTGGTCAATGTATGTGATTGTCAAGATACACCAAGAT
GAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGATGCCCTAGCCACCAAGTACCCTGCCCTTTCAGAGT
GTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTTTGCAAGATAGTATCTCCATAGATTACTATAACATGT
TCACGAGCATATTCACCCCTCTGCACCATGAGTGTGATCGATACATTGCAGTCTGCCACCTGTCAAGGCCTTAGATTTC
CGTACTCCCCGAAATGCCAAATTATCAAATGTCTGCAACTGGATCCTCTCTTCAGCCATTGGTCTTCCTGTAATGTTCA
GGTACAAACAAATACAGGCAAGGTTCCATAGATTGTACACTAACAATCTCTCATCCAAACCTGGTACTGGGAAACCTG
CTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTGTCTCATCATACCGTGTGCTATGGACTGATGATCTTGG
CCTCAAGAGTGTCCGATGCTCTCTGGCTCCAAAGAAAGGACAGGAATCTTCGAAGGATCACCAGGATGGTGTGGT
GGTGTGGCTGTGTTCACTGTCTGTGGACTCCCATTCACATTTACGTCACTAATTAAGCCTTGGTTACAAATCCCAAGAA
CTACGTTCCAGACTGTTTCTTGGCACTTCTGCACTTCTAGGTTACACAAACAGCTGCCTCAACCCAGTCTTTATGCA
TTTCTGGATGAAAACCTCAACGATGCTTCAGAGAGTCTGTATCCCAACCTCTTCCAAACATTGAGCAACAAACTCCA
CTCGAATTCGTCAAGAACACTAGAGACCCCTCCACGGCCAATACAGTGGATAGAACTAATCATCAGAAAAATAGATT
TATTTCAAAAGTCACTTTACTCAACTGTGAGCATACCAAGGGCTAATAATTACAATATTTTCCCGTGAAAGATATAA
GATTGGAAAGC (SEQ ID NO:50)

hMOR-1B1 (406 aa)

MDSSAAPTNASNCTDALAYSSCPAPSPGSWVNLSHLDGNLSDPCGNRITDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRIITRMVLVVVAVFIVCWTPIHIVYVIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRITNHQKIDLFQKSSLLNCEHTKG (SEQ ID NO:51)

FIG. 3A

hMOR-1B2 (2218 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGCGCTCAGTACCATGGACAGCAGCGCTGCCCCACGAACG
CCAGCAATTGCACTGATGCTTGGCGTACTCAAGTTGCTCCCGACGACCCAGCCCCGTTCTGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATCGGTCGGAACCGCACCGACTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCAGATCATGGCCCTCTACTCCATCGTGTGCGTGGTGGGCTCTTCGGAAAC
TTCCTGGTCAATGTGATTGTGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGTCTTGGC
AGATGCCCTTAGCCACCAAGTACCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTGGAACCATCCTT
TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTTCCAGCATATTACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCTTAGATTTCGGTACTCCCGAAATGCCAAATTTATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCTGTAAATGTTTCATGGCTACAAACAAATACAGGCAAGTTCCATAGATTGTACAC
TAACATTTCTCTCATCCAACTGGTACTGGGAAACCTGTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTG
CTCATCTTACCGTGTGCTATGGAATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAGG
ACAGGAATCTTCGAAGGATCACCAAGGATGGTGTGGTGGTGGTGTGTTTCATCGTCTGTGTGGACTCCCATTCACAT
TTACGTCACTAATAAGCCTTGGTTACAATCCAGAAACTACGTTCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAACAGCTGCCTCAACCCAGTCTTTATGCAATTTCTGGATGAAACTTCAAAACGATGCTTCAGAGAGTTCTG
TATCCAACTCTTCCAACATTGAGCAACAAACTCCACTCGAAATTCGTCAAGAACACTAGAGACCAACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGAGAGAAAGAACAGAAATCTGACTGGTAAGAAATTTGTACCCCTTTTGCCA
GCATGCCAGGCTTCTGGGTCCCTTTCCCTGAGCGGCCCTAGTGATCCGGCTTGGCGACCATCGCCTACGGGCCAAGC 6/26
TGCA TCATAAAGGAAATTTTTTTTTCATTCTGGCCAGAGCAAAACACATGTGATAAAACATAGGCATTAGCTACTCTG
CTTAGCACCAATATCAGACTAGCTTAAATTTGCCCCCAGATGGGTTCCATCATCTTTAATCCGACCTCTGACTTGCAGT
TTCAACACGTCTCTTTGGCAAAACAGTTGCCCTGAGTAACAGAAAGATAGGAAAGGAAAGGAGAGAGAGAAA
AATGTGCCCAGTGGAAAGGTGGGGAAGTGAAATGATCAAGGAGCCAGAGAAAGACTCACCTATTGCAGCAACACT
GTAGAAGTTCAGGCACTGCTTCTCGGTAGCAAAAGGATCTTTTCCAGCAATCTTATTAGCTCTCAAGTTTCCCCCTTTTA
GGGAGGAAAAAGCTCCCAATGTCCCGCGATCCTGTACATGTCTCAACCTGCCATCCACAGCCATCAGCAAGAGTGCA
AGACAGATTAAATCCAAAGAGAAATAGCAATTAATATCCCATAGCATCAAAGCTGTTCTTAGCCAAAGAGGACTTTAAACG
GGAGGGGTCTCTAACACCCCTAAATCTTAGAAGAGACTTAACCATCTTAAGTAGGGCCTCTAACCCCGCTTTATAAAT
TTTAATTGACTCCCATCTTAACAGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAGATAAAACCAAGC
ATACTAGAAAGTGTCTCTAAATTAATAATACAGTAGTTGCTAGAGAAAAATTTTAGTCCAAAAATCCAACTATAGAA
ACATAGAAATGTGAGAGGTAGCACATAAGAAATAAGTCAATGGGGATTTTATTTCATGGACCAGCAATATGATGATAAAA
GCCATCTAACCC (SEQ ID NO:52)

FIG. 3B(1)

hMOR-1B2 (397 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITIMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWNLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVAVFIVCWTPIHYYVIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIP TSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQRRRQKSDW
(SEQ ID NO:53)

7/26

FIG. 3B(2)

[illegible]

GTCCAAAATCCAACTATAGAAACATAGAAATGTGAGAGGCAGCACATAAGAAAATAAGTCATGGGGATTTTATTTCAT
GGACCAGCAATATGATGATAAAAGCCATCTAACC (SEQ ID NO:54)

hMOR-1B3 (403 aa)

MDSSAAPTNASNCITDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWLSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPIHYYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQPPAKFVADQLAGSS (SEQ ID NO:55)

9/26

FIG. 3C(2)

hMOR-1B4 (1251 bp)

CGGTGCTCCTGCTACCTCGCACAGCGGTGCCCGCCGGCGTCACTACCATGGACAGCGCTGCCCGCCACGAACG
CCAGCAATTGCACTGATGCCCTGGCGTACTCAAGTTGCTCCCCAGCACCCAGCCCGGTTCTTGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCAGGCCATCACGATCATGCGCCCTCTACTCCATCGTGTGCGTGGGGCTCTTCGGAAAC
TTCTGGTCATGTATGTGATTGTCAGATACACCAAGATGAAGACTGCCACCAACATCTACGTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAAGTACCCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCAATTTGGAACCATCCTT
TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTACACGACATATTCAACCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCGGTACTCCCCGAAATGCCAAATATCAATGTCTGCAACTG
GATCCTCTTCAGCCATTGGTCTTCTGTAAATGTTTCATGGCTACAAACAAATACAGGCAAGTTCCATAGATTGTACAC
TAACATTCTCTCATCCAACTGTGTTACTGGGAAACCTGTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTG
CTCATCATACCGTGTGCTATGGACTGATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAGG
ACAGGAATCTTCGAAGGATCACCAAGATGGTGTGGTGGTGTGTTTCATCGTCTGTGGACTCCCATTCACAT
TTACGTCAATCAATAAGCCTTGTTACAAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAAACAGCTGCCCTCAACCCAGTCTTTATGCATTTCTGGATGAAACTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAAACATTGAGCAACAAACTCCACTCGAATTCTGTCAGAACACTAGAGACCAACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGAGCTGACTATGACATGAACCCCTAAATTCCTGTTCCC (SEQ ID NO:56)

hMOR-1B4 (389 aa)

MDSSAAPTNASNCTDALAYSSCAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNELVMYVIVRYTKMKTATNIYVFNLAADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYVNNMFTSIFTLCTMSVD
RYIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIIT
VCYGLMILRLKSVRMLSGSKEKDRNLRRJTRMVLVVVAVFIVCWTPHIYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNP
VLYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQ (SEQ ID NO:57)

FIG. 3D

CGGTGCTCTGGCTACCTCGCACAGCGGTGCCCCGCCGCTCAGTACCATGACACGACGCGCTGCCCCACGAAACG
CCAGCAATTGCACTGATGCCTTGGGTACTCAAGTTGCTCCCCAGCACCCAGCCCCGTTCTCTGGTCAACTTGTCCCCA
CTTAGATGGCAACCTGTCCGACCCATGGGTCCGAACCGCACCGACCTGGGGGGGAGACAGCCTGTGCCCCCTCCGAC
CGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGTGGGGCTCTTCGGAAAC
TTCTGGTCATGTATGTGATGTCAGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAGTACCTGCCCTTCCAGAGTGTGAATTAACCTAATGGGAACATGGCCATTTGGAAACCATCCTT
TGCAAGATAGTAGTCTCCATAGATTACTATAACATGTTCAACCAGCATATTTACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCTTAGATTTCCGTACTCCCCGAAATGCCAAAATTATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCTGTAAATGTTTCATGGCTACAACAAATAACAGGCAAGTTCCATAGATTGTACAC
TAACATTTCTCATCCAACCTGGTACTGGGAAAACCTGTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGACTGATGATCTTGGCGCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAAGAAAGG
ACAGGAATCTTCGAAGGATCACCGATGGTGTGGTGGTGGTGTGTTTCATCGTCTGTGACTCCCATTCACAT
TTACGTCTCATTAATAAGCCTTGGTTACAAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAAACAGCTGCTCAACCCAGTCTTTATGCAATTTCTGATGAAAACCTTCAAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAAACATTGAGCAACAAACTCCACTCGAATTCGTCAGAACTAGAGACCAACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGGTGGAAATTGAACCTGGACTGTCACTGTGAAATATGCAAAGCCTTGGCCACTG
AGCTACAAATGCAGGGTAGTCTCCATTTCCCTTCCCAGGAAGAGTCTAGAGCGTTAAATTTTGAGTTTTCGAAAGGCTTGA
ACTATTTTCATATGATTTTAGAGCTGACTATGACATGAACCCCTAAAATTCCTGTTCCC (SEQ ID NO:58)

hMOR-1B5 (410 aa)

FIG. 3E

[illegible]

12/26

AGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAAACCAAGCATAGAGTGTCTCTAAA
ATTAAAAATACAGTAGTTGCTAGAGAAAAATTTAGTCCAAAAATCCAACTATAGAAACATAGAAATGTGAGAGGTAGC
ACATAAGAAAAATAAGTCATGGGGATTTTATTTTCATGGACCAGCAATATGATGATAAAAGCCATCTAACCAAGGGC
(SEQ ID NO:60)

hMOR-1Y (402 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITIMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNLYLMGTWPFGTILCKIVISIDYYNMFSTIFTLCTMSVDR
YIACHPVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVAVFIVCWTPHIYVVIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIP TSSNIEQQNSTRQNTNRDHPSTANTVDRTNHQIRDPISNLP RVSVF (SEQ ID NO:61)

hMOR-1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1A (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B2 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B3 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B4 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B5 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1O (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1X (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1Y (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
Consensus (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP

61

120

hMOR-1 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1A (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B1 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B2 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B3 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B4 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B5 (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1O (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1X (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1Y (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
Consensus (61) PTGSPSMITAITIMALYSIVCVWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT

FIG. 4(1)

	121	180
hMOR-1	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1A	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1B1	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1B2	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1B3	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1B4	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1B5	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1O	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1X	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
hMOR-1Y	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
Consensus	(121)	STLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRIYAVCHPVPKALDF
	181	240
hMOR-1	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1A	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B1	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B2	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B3	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B4	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B5	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1O	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1X	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1Y	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
Consensus	(181)	RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI

FIG. 4(2)

	241		300
hMOR-1	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1
hMOR-1A	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1A
hMOR-1B1	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1B1
hMOR-1B2	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1B2
hMOR-1B3	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1B3
hMOR-1B4	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1B4
hMOR-1B5	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1B5
hMOR-1O	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1O
hMOR-1X	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1X
hMOR-1Y	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	hMOR-1Y
Consensus	(241)	FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVWAVFIVCWTP	
	301		360
hMOR-1	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1
hMOR-1A	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1A
hMOR-1B1	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1B1
hMOR-1B2	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1B2
hMOR-1B3	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1B3
hMOR-1B4	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1B4
hMOR-1B5	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1B5
hMOR-1O	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1O
hMOR-1X	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1X
hMOR-1Y	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	hMOR-1Y
Consensus	(301)	YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFDENFKRCFREFCIPTSS	

FIG. 4(3)

361	420	
hMOR-1 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQLENLEAETAPLP-----	
hMOR-1A (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQVRSL-----	
hMOR-1B1 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLLNCEHTKG-----	
hMOR-1B2 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQRERRQKSDW-----	
hMOR-1B3 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS-----	
hMOR-1B4 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQS-----	
hMOR-1B5 (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG-----	
hMOR-1O (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQPPLAVSMAQIFTRYPPPTHREKTCNDYMKR--	
hMOR-1X (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQCLPIPSLSCWALEHGCLVYPGPLQGPLVRYD	
hMOR-1Y (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSF-----	
Consensus (361)	EQQNSTRIRQNTRDHPSTANTVDRTNHQ	

421	446	
hMOR-1 (401)	-----	(SEQ ID NO:62)
hMOR-1A (393)	-----	(SEQ ID NO:63)
hMOR-1B1 (407)	-----	(SEQ ID NO:51)
hMOR-1B2 (398)	-----	(SEQ ID NO:53)
hMOR-1B3 (404)	-----	(SEQ ID NO:55)
hMOR-1B4 (390)	-----	(SEQ ID NO:57)
hMOR-1B5 (411)	-----	(SEQ ID NO:59)
hMOR-1O (419)	-----	(SEQ ID NO:64)
hMOR-1X (421)	LPAILHSSCLRGNTAPSPGGAFLLS (SEQ ID NO:65)	
hMOR-1Y (403)	-----	(SEQ ID NO:61)
Consensus (388)		(SEQ ID NO:66)

FIG. 4(4)

rMOR-1A

Exon 3a ↓ Exon 3b

-----AACCACCAGGTATGTGCTTTCTAGAATTACGGATAACATATAAAAAATACCATATCTGGTA

N H Q V C A F * (SEQ ID NO:67)

CCAGTCTAAGATTAAATCTTTAAGAAGGTCAGTAACTTGAGGCAAAAGTCC (SEQ ID NO:68)

rMOR-1C1

Exon 3a ↓ Exon 7

-----AACCACCAGCCAGCCCTGGCAGTCAGCGTGGCCCGAGATCTTTACAGGATATCCTTCTCCG

N H Q P A L A V S V A Q I F T G Y P S P

↓ Exon 8

ACTCATGGTGAAAAACCCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAGAACGTGGT

T^D H G E K P C K S^D Y R D R P R P C G R T W

CTTTGAAATCGCGTGCAGAATCCAATGTGGAGCACTTCCATTGTGGAGCCGCATTAAATCTATAA

S⁺ L K S^D R A E S^D N V E H F H C G A A L I Y N

↓ Exon 9a

CAATGTGAATTTTCATCTAAACACAGGGATGTGCTAGTGAGAAAGTTTGGAGGTGCAGGC (SEQ ID NO:69)

N V N F I * (SEQ ID NO:70)

FIG. 5(1)

rMOR-1C2

Exon 3a ↓ Exon 7

-----AACCACAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCG
 N H Q P A L A V S V A Q I F T G Y P S P

↓ Exon 8

ACTCATGGTGAAAAACCCCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAGAACGTGGT
^{T^D} H G E K P C K ^{S^D} Y R D R P R P C G R T W
 CTTTGAAATCGCGTGCAGAATCCAATGTGGAGCACTTCCATTGTGGAGCCGCAATTAATCTATAA
^{S⁴} L K ^{S^D} R A E ^{S^D} N V E H F H C G A A L I Y N

↓ Exon 9b

CAATGAACATAAAATAGGGCCAGTGTCTGGTCCAGATGCCTGCGCACGTGCTCGTGGCCCCC
 N E L K I G P V S W L Q M P A H V L V R P
 TGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:71)
 W * (SEQ ID NO:72)

rMOR-1D

2 4 6

Exon 3a ↓ Exon 8

-----AACCACAGACCTAGACCCCTGTGGAAGAACGTGGTCTTTGAAATCGCGTGCAATCCAA
 N H Q T * (SEQ ID NO:73) ↓ Exon 9b

TGTGGAGCACTTCCATTGTGGAGCCGCATTAAATCTATAACAATGAACATAAAAAATAGGGCCAGTG
 TCCTGGCTCCAGATGCCCTGCGCACGTGCTCGTGGCCCCCTGGTAATGAACACGGGCTCCGATT
 TGAATATCCTTCTGTG (SEQ ID NO:74)

FIG. 5(2)

Exon 3a ↓ **Exon 5b**
 -----AACCACCGAGGCTCAGTCAGTAGAGACATGATGTGAATGAACCAACTGATTAACAAG
 N H Q E P Q S V E T * (SEQ ID NO: 75)
 GTTTTCTGAACACTGAAATACAACACAAAATGTAGAGGTTACTAGAGAAAATTTGTAGCCTGAAAATTCAATTACGGAAACCAAATGAGT
 GTGAGTGATACATTTTAAAGGCCTCAGAGAGATTTATTTCATGACTAACAAACATGACCCAAAGCACCTAAACTGTGGTGATTAGATTA
 CAAAGACAATTTCTAGAGCCTGGGACTAAAGAAATGTTAGCCCTCACACAGACAGGCCTCACACTTCAGTAATGGAATGAGCAAATTAGA
 TTAGTGAGAAAGATGGAGGAAAGACTCGAAATATTTTCATATCTTCCTGTGGAACCTCCACAGAAAAACCAATAGAATAAACCAACCTGC
 TGGACCCCTGGTGGCTCTTACC (SEQ ID NO: 76)

[illegible]

rMOR-1B2 (1628 bp)

GTTACAGCCTACCTAGTCCGCGAGCAGGCCCTTCAGCACCATGGACAGCAGCACCGGCCAGGGAACACAGGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTGTCCCACGTTGATGGCAACCAAGTC
CGATCCATGCGGTCTGAACCGCACCGGCTTGCGGGAAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGGT
CACAGCCATTACCATCAATGCGCCCTCTACTCTATCGTGTGTAGTGGGCTCTTCGGAAACTTCCTGGTCATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTCTGCTGGCAGACGCCCTTAGCGACCCAG
TACACTGCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATTCA
ATAGATTACTACAACATGTTTCCAGCATATTCACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCCGTACCCCCGAAATGCCAAAATCGTCAACGTCTGCAACTGGATCCCTCTCTTCTGCCAT
CGTCTGCCGTGTAATGTTTCATGGCAACCAAAAATACAGGCAAGGTCCATAGATTGCAACCTCACGTTCTTCCCACCCA
ACCTGGTACTGGGAGAACCTGCTCAAAAATCTGTGCTTTATCTTCGCTTTCATCATGCCGTCTCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTTCGCATGCTATCGGCTCCAAAAGAAAGGACAGGAATTTGCCGAG
GATCACCCGGATGGTGGTGGTGGTGTATTTATCGTCTGTGGACCCCTCCACATCTACGTCAATCAACAA
GGCTGATCACGATTCAGAAACCAATTCAGACCGTTTCTGGCACTTCTGCAATGCTTGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTTACGCCCTTCTGGGATGAAACTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTC
GTCCACGATCGAAACAGCAAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGA
TCGAACTAACCAAGGAGCCTCAGTCAGTAGAGACATGATGTGAATGAACCAACTGATTAAACAAGGTTTCTGAAC
ACTGAAATACAAACACAAATGTAGAGGTTACTAGAGAAAATTTGTAGCCTGAAAATTTCAATTACGGAACCAAAATGAGT
GTGAGTGATACATTTTAAGGCCTCAGAGAGATTTTATTTCAATGACTAAACATGACCCAAAGCACCTAAACTGTGGT
GATTAGATTACAAGACAAATTCAGAGCCTGGACTAAAGAAATGTTAGCCCTCACACAGACAGGCCCTCACACTTCAG
TAATGGAAATGACCAATTAGATTAGTGAGAAAGATGGAGGAAAGACTCGAAATATTTTCATATCTTCTGTGGAACTC
CACAGAAAACCAATAGAAATAAACCAACCTGCTGGACCCCTTGGTGGCTCTTACC (SEQ ID NO:79)

rMOR-1B2 (394 aa)

MDSSTGPGNTSDCSDPLAQASCSPAPGSWLNLSHVVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFILCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFVVCWTPHIYVIAKALITPETTFQTVSWHFCIALGYTNSCLNPVL
LRLPGMKTSSDASEEFCIPTSTIEQQNSTRVQRNTRHPSTANTVDRTNHQEPQSVET (SEQ ID NO:80)

FIG. 6A

rMOR-1C1 (1433 bp)

GTTACAGCCTACCTAGTCCGCAGCAGGCCCTTCAGCACCATGGACAGCAGCACCGGCCACAGGAACACAGGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTGTGCCACGTTGATGGCAACCAAGTC
CGATCCATGCGGTCTGAACCGCACCGGCTTGGCGGAACGACAGCCTGTGCCCTCAGACCGGCAAGCCCTTCCATGGT
CACAGCCATTACCATCATGCGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAACTTCCTGGTCAATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACACAG
TACACTGCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTACACGACATATTCAACCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCGTACCCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTCTCTGCCAT
CGGTCTGCCCTGTAATGTTTCATGGCAACCAAAATACAGGCGGGTCCATAGATTGCACCCCTACGTTCTCTCCACCCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGTCTTTATCTTCGCTTTCATCATGCCGTCTCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTTCGATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCCGAG
GATCACCGGATGTGCTGTTGCTGCTGATTTATCGTCTGTGGACCCCTCCACATCTACGTCAATCAATA
GCGTGATCACGATCCAGAAACCAATTCAGACCGTTTCTGGCACTTCTGCACTTGTGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTACGCTTCTCTGGATGAAACTTCAAGCATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCC
ACGATCGAACAGCAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCCAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCGACTCATGGTGAATAAC
CCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAGAACGTGGTCTTTGAAATCGCGTGCAGAAATCCAATGTGG
AGCACTTCCATTGTGGAGCCGCATTAACTATAACAATGTGAATTTTCATCTAAACACAGGGATGTGCTAGTGAGAAATT
TGGAGGTGCAGGC (SEQ ID NO:81)

rMOR-1C1 (451 aa)

MDSSTGPGNTSDCDPLAQASCPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVAVFVVCWTPHIHYVIAKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPKCKSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNVNF1 (SEQ ID NO:82)

FIG. 6B

rMOR-1C2 (1480 bp)

GTTACAGCCTACCTAGTCCGCAGCAGGCCTTCAGCACCATGGACAGCAGCACCGGCCAGGGAACACACGAGCTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCGACACCTGGCTCCTGGCTCAACTTGTCCACCGTTGATGGCAACACGATC
CGATCCATGCGGTCTGAACCGCACCCGGCTTGGCGGAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGGT
CACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAAACTTCCTGGTCATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGTCTGGCAGACGCCCTTAGCGACCCAG
TACACTGCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTCAACGACATATTCAACCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCGGTACCCCGGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCCTCTCTTCTGCCAT
CGGTCTGCCCTGTAATGTTTCATGGCAACCAAAATACAGGACGGGTCCATAGATTGCAACCTCACGTTCTCTCCACCCA
ACCTGTACTGGGAACCTGTCTCAAAATCTGTGTCTTTATCTTCGCTTTCATCATGCCGTCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGGCGCAG
GATCACCGGATGGTGTGGTGGTGTATTTATCGTCTGTGTGACCCCATCCACATCTACGTCTCATCAATAA
GCGTGTACGATCCAGAAACCAATTTTCAGACCGTTTCTGGCACTTCTGTGCTTGGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTACGCTTCTCTGGATGAACCTCAAGCGATGCTTCAGAGAGTTCGTGCATCCCAACCTCGTCC
ACGATCGAACAGCAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCAACAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCGACTCATGGTGAAAAAC
CCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAGAACGTGTCTTTGAAATCGCGTGCAGAAATCCAATGTGG
AGCACTTCCATTGTGGAGCCGCATTAATCTATAACAATGAACATAAATAGGGCCAGTGTCTGGCTCCAGATGCCTGC
GCACGTGCTCGTGGCCCCCTGGTAATGAACACGGGCTCCGATTCTGAAATATCCTTCTGTG (SEQ ID NO:83)

23/26

rMOR-1C2 (468 aa)

MDSSTGPGNTSDCDPLAQASCSPAPGSWNL SHVDGNQSDPCGLNRTGLGGNDLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSLPFSQSVNYLMGTWPFGTILCKIVISIDYYNMFSTIFTLCTMSVDY
IAVCHPVKALDFRTPRNAKIVNCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVVAVFVVCWTPHIYVVIKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPSTSTIEQQNSTRVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPKCKSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNELKIGPVSWLQMPAHVLVRPW (SEQ ID NO:84)

FIG. 6C

rMOR-1D (1385 bp)

GCCTACCTAGTCCGCAGCAGGCCCTTCAGCACCATTGGACAGCAGCACCGGCCACGGGAACACCAAGCGACTGCTCAGACC
CCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTTGTCCACGTTGATGGCAACCAAGTCCGATCC
ATGCGGTCTGAACCGCACCGGGCTTGGCGGAACGACAGCCCTGTGCCCTCAGACCGGACGCCCTTCCATGGTCACAGC
CATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAAACTTCTCTGGTCAATGATGTGATTGTAA
GATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGTCTGGCAGACGCCCTTAGCGACCAAGTACACT
GCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCAATAGAT
TACTACAACATGTTCAACCAAGCATATTCACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACCCAGTCA
AAGCCCTGGATTTCCGTACCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCATCGGTCT
GCCTGTAATGTTTCATGGCAACCAACAAATACAGGCAGGGGTCCATAGATTGCAACCTCACGTCTCTCCACCCAAACCTGG
TACTGGGAGAACCTGCTCAAAATCTGTGCTTTGCTTCGCTTTCATCATGCCGGTCCCTCATCATCACTGTGTGTACGG
CCTGATGATCTTACGACTTAAGAGCGTTCCGATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAGGATCAC
CCGGATGGTGTGGTGTGGTGTATTTATCGTCTGTGGACCCCATCCACATCTACGTCAATCAAAAGCGCTG
ATCACGATTCCAGAAACCAATTTTCAGACCGTTTCTCGCACTTCTGCAATTGCTTTGGGTTACACGAACAGCTGCCTGA
ATCCAGTTCTTACGCCCTTCCCTGGATGAAACTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCCACGATC
GAACAGCAAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGAACTAAC
CACAGACCTAGACCTGTGGAAAGAACGTGGTCTTTGAAATCGCGTGCAGAAATCCAAATGTGGAGCACTTCCATTGTGGA
GCCGCATTAACTATAACAATGAACTAAATAGGGCCAGTGTCTGGCTCCAGATGCCCTGCGCACGTCGTCGTGCGCC
CCTGGTAATGAACACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:85)

24/26

rMOR-1D (387 aa)

MDSSTGPGNTSDCDPLAQASCSPAPGSWNLNLSHVDGNQSDPCGLNRTGLGGNDLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFVFAFIMPVLHIV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVVAVFIVCWTPHIYVIAKALITPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCREFCIPTSSTIEQQNSTRVQRNTREHPSTANTVDRTNHQT (SEQ ID NO:86)

FIG. 6D

27

25/26

CCAGCACATTCCTGTTTC (SEQ ID NO:87)

rMOR-1E (390 aa)

MDSSSTGPGNTSDCSDPLAQASCPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKA'TNIYFNLAADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLITV
CYGLMILRLKSVRM LSGSKEKDRNLRGITRMVLVVAVFVVCWTPHIYVIAKALITIPETTFQT VSWHFCIALGYTNSCLNPVL
YAFLDENFKRCREFCIPTSSTIEQQNSTRVQRNTREHPSTANTVDRTNHQGAEL (SEQ ID NO:88)

26/26

FIG. 6E(2)